SEQUENCE LISTING

<110> Wei et al.

<120> Human Hematopoietic - Specific Protein

<130> PF268D1C1

<150> PCT/US96/04930
<151> 1996-04-11

<150> 08/837,029
<151> 1997-04-11

<150> 09/265,977
<151> 1999-03-11

<160> 8

<170> PatentIn version 3.1

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<212> DNA
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                                              Met Arg Leu Ser Leu
                                                             -20
cca ctg ctg ctg ctg ctg ctg gga gcc tgg gcc atc cca ggg ggc ctc      104
Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile Pro Gly Gly Leu
        -15                 -10                 -5
ggg gac agg gcg cca ctc aca gcc aca gcc cca caa ctg gat gat gag      152
Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln Leu Asp Asp Glu
-1  1               5                   10                  15
gag atg tac tca gcc cac atg ccc gct cac ctg cgc tgt gat gcc tgc      200
Glu Met Tyr Ser Ala His Met Pro Ala His Leu Arg Cys Asp Ala Cys
                20                  25                  30
aga gct gtg gct tac cag atg tgg caa aat ctg gca aag gca gag acc      248
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Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu Ala Lys Ala Glu Thr
            35                  40                  45
aaa ctt cat acc tca aac tct ggg ggg cgg cgg gaa ctg agc gag ttg      296
Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg Glu Leu Ser Glu Leu
        50                  55                  60
gtc tac acg gat gtc ctg gac cgg aac tgc tcc cgg aac tgg cag gac      344
Val Tyr Thr Asp Val Leu Asp Arg Asn Cys Ser Arg Asn Trp Gln Asp
    65                  70                  75
tac gga gtt cga gaa gtg gac caa gtg aaa cgt ctc aca ggc cca gga      392
Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg Leu Thr Gly Pro Gly
80                  85                  90                  95
ctt agc gag ggg cca gag cca agc atc agc gtg atg gtc aca ggg ggc      440
Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val Met Val Thr Gly Gly
                100                 105                 110
ccc tgg cct acc agg ctc tcc agg aca tgt ttg cac tac ttg ggg gag      488
Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu His Tyr Leu Gly Glu
            115                 120                 125
ttt gga gaa gac cag atc tat gaa gcc cac caa caa ggc cga ggg gct      536
Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln Gln Gly Arg Gly Ala
        130                 135                 140
ctg gag gca ttg cta tgt ggg gga ccc cag ggg gcc tgc tca gag aag      584
Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly Ala Cys Ser Glu Lys
    145                 150                 155
gtg tca gcc aca aga gaa gag ctc tagtcctgga ctctaccctc ctctgaaaga     638
Val Ser Ala Thr Arg Glu Glu Leu
160                 165
agctggggct tgctctgacg gtctccactc ccgtctgcag gcagccagga gggcaggaag    698
cccttgctct gtgctgccat cctgcctccc tcctccagcc tcagggcact cgggcctggg    758
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aaaaaaaaaa aaaaa                                                    833
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<210> 2
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<213> human

<400> 2

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Met Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala
        -20                 -15                 -10

Ile Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro
    -5              -1  1               5                   10

Gln Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu
                15                  20                  25

Arg Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu
            30                  35                  40

Ala Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg
        45                  50                  55

Glu Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Asn Cys Ser
    60                  65                  70

Arg Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg
75                  80                  85                  90

Leu Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val
```

95 100 105

Met Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu
110 115 120

His Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln
125 130 135

Gln Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly
140 145 150

Ala Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
155 160 165

<210> 3
<211> 28
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing a Bam HI restriction site encoding a start AUG, followed by 19 nucleotides of the hHSP coding sequence beginning with the first base of the 23rd codon.

<400> 3
cgcggatccg acagggcgcc actcacag 28

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing an Xba I restriction site followed by 21 nucleotides complementary to the last 21 nucleotides of hHSP including the stop codon.

<400> 4
gcgtctagag aggtcactgg gttttatttg 30

<210> 5
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing a Bam HI restriction site followed by 19 bases of the sequence of hHSP.

<400> 5
cgcggatccg ccatcatgag gctgtcactg ccac 34

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing an Xba I restriction site

followed by nucleotides complementary to the last 21 nucleotides of hHSP including the stop codon.

<400> 6
gcgtctagag aggtcactgg gttttatttg 30

<210> 7
<211> 34
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing a Bam HI site, an AUG start codon and 16 nucleotides thereafter.

<400> 7
cgcccatccg ccatcatgag gctgtcactg ccac 34

<210> 8
<211> 57
<212> DNA
<213> Artificial Sequence
<220>
<221> Primer_Bind
<223> Synthetic primer containing an Xba I site, a stop codon, 9 codons forming hemaglutinin tag and 18 bp of 3' coding sequence.

<400> 8
cgctctagat caagcgtagt ctgggacgtc gtatgggtag agctcttctt ctgtggc 57